SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Chatterjee, Malaya
           Foon, Kenneth A.
           Chatterjee, Sunil K.

   (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
        11D10 AND METHODS OF USE THEREOF

  (iii) NUMBER OF SEQUENCES: 58

   (iv) CORRESPONDENCE ADDRESS:
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        (F) ZIP: 94304-1018

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

   (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US
        (B) FILING DATE:
        (C) CLASSIFICATION:

 (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Polizzi, Catherine M.
        (B) REGISTRATION NUMBER: 40,130
        (C) REFERENCE/DOCKET NUMBER: 30414-20003.21

   (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (415) 813-5600
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        (C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 435 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA      48
Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
-20             -15             -10                         -5

GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT      96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
                1               5               10

GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC     144
Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
        15              20              25

ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT     192
Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
        30              35              40

AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA     240
Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
45              50              55              60

AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC     288
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
                65              70              75

AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT     336
Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
                80              85              90

AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG     384
Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        95              100             105

GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT     432
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
    110             115             120

GGG                                                                 435
Gly
125
```

(2) INFORMATION FOR SEQ ID NO:2:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
-20               -15              -10                       -5

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
                1                5                   10

Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
        15                  20              25

Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
    30              35              40

Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
45              50              55                      60

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
            65              70                      75

Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
            80              85              90

Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        95              100             105

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
    110             115             120

Gly
125
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 461 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..459

    (ix) FEATURE:
        (A) NAME/KEY: mat_peptide
        (B) LOCATION: 58

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT        48
Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
-19             -15                 -10                     -5
```

3

```
GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG        96
Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
            1               5               10

TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG        144
Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
    15              20              25

ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG        192
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
30              35              40              45

GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT        240
Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
            50              55              60

CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC        288
Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
            65              70              75

ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC        336
Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
        80              85              90

TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT        384
Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
    95              100             105

CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC        432
Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
110             115             120             125

GTC TAT CCA CTG GTC CCT GGA AGC TTG GG                                 461
Val Tyr Pro Leu Val Pro Gly Ser Leu
            130
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 153 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
-19             -15             -10             -5

Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
            1               5               10

Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
    15              20              25

Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
```

4

Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
                 50   55   60

Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
             65   70   75

Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
         80   85   90

Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
     95   100   105

Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
110   115   120   125

Val Tyr Pro Leu Val Pro Gly Ser Leu
                 130

(2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 321 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT   60

CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA   120

GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTGCCCAAA   180

AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT   240

GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG   300

GGGACCAAGC TGGAAATAAA A   321

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 321 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GANATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT        60

CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA       120

GATGGAACTT TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA       180

AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT       240

GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT GTCCGTACAC GTTCGGAGGG       300

GGGACCAAGC TGGAAATAAA A                                                 321
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 321 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT        60

CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA       120

GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA       180

AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT       240

GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA       300

GGCACCAAGC TGGAAATCAA A                                                 321
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 321 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT        60

CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA       120
```

GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA   180

AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT   240

GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA   300

GGCACCAAGC TGGAAATCAA A   321

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 321 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT   60

CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA   120

GATGGAACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA   180

AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT   240

GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA   300

GGCACCAAGC TGGAAATCAA A   321

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 318 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCCAGATGA CCCAGTCTCC ATCCTCCTTA TCTGCCTCTC TGGGAGAAAG AGTCAGTCTC   60

ACTTGTCGGG CAAGTCAGGA CATTGGTAGT AGCTTAAACT GGCTTCAGCA GGAACCAGAC   120

GGAACTATTA AACGCCTGAT CTACGCCACA TCCAGTTTAG ATTCTGGTGT CCCCAAAAGG   180

TTCAGTGGCA GTAGGTCTGG GTCAGATTAT TCTCTCACCA TCAGCAGCCT TGAGTCTGAA   240

GATTTTGTAG ACTATTACTG TCTACAATAT GCTAGTTCTC CGTGGACGTT CGGTGGAGGC   300

ACCAAGCTGG AAATCAAA   318

(2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 303 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCATCCT CCTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT   60

CAGGACATTG GTAGTAGCTT AAACTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC   120

CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTCAG TGGCAGTAGG   180

TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAGT CTGAAGATTT TGTAGACTAT   240

TACTGTCTAC AATATGCTAG TTCTCCGTAC ACGTTCGGAG GGGGGACCAA GCTGNAAATA   300

AAA   303

(2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 321 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT   60

CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGTTACTTAA GCTGGCTTCA GCAGAAACCA   120

GATGGAACTA TTAAACGCCT GATCTACAGC ACATCCACTT TAAATTCTGG TGTCCCAAAA   180

AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT   240

GAAGATTTTG CAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG   300

GGGACCAAAC TGGAAATAAA A   321

(2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 303 base pairs

                                    8

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCTCCATCCT CCTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT   60

CAGGACATTG GTAATAGCTT AAACTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC   120

CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTCAG TGGCAGTAGG   180

TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAAT CTGAAGATTT TGTAGTCTAT   240

TACTGTCTAC AATATGCTAG TTATACGTAC ACGTTCGGAG GGGGGACCAA GTTGGAACTA   300

AAA   303

(2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 321 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT   60

CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGTTACTTAA GCTGGCTTCA GCAGAAACCA   120

GATGGAACTA TTAAACGCCT GATCTACGCC GCATCCACTT TAGATTCTGG TGTCCCAAAA   180

AGGTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT   240

GAAGATTTTG CAGACTATTA CTGTCTACAA TATCTTAGTT ATCCGCTCAC GTTCGGTGCT   300

GGGACCAAGC TGGAGCTGAA A   321

(2) INFORMATION FOR SEQ ID NO:15:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 294 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGCTTATN TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG   60

TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA   120

CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC   180

AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC   240

ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGA   .   294

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA   46

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 360 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGGCTTATG TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG   60

TCCTGCAAGG CTTCTGGCTA CAGATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA   120

CGTAGACAGG GCCTGGAATG GATTGGAGCA ATTTATCCAG GAAATGGTGA TACTTCCTAT   180

AATCAGAAGT TCAAGGGCAA GGCCACACTG ATTGTAGACA AATCCTCCAG CACAGCCTAC   240

ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGAGAGG   300

GGTAACTACG TAGGACATAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC CGTCTCCTCA   360

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 354 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTAAGGC CTGGGTCCTC AGTGAAGATG   60

TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA   120

CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC   180

AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC   240

ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGGGGAT   300

TACTCCGGTA GTATAGACTA CTGGGGCCAA GGCACCACTC TCACAGTCTC CTCA   354

(2) INFORMATION FOR SEQ ID NO:19:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 297 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG   60

TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA   120

CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC   180

AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC   240

ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG   297

(2) INFORMATION FOR SEQ ID NO:20:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTGGGGCACA GGGACCACGG TCACCGTCTC C   31

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 297 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG   60

TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA   120

CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC   180

AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC   240

ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG   297

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGGGGCACA GGGACCACGG TCACCGTCTC   30

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 300 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGGTCCAGCT GCAGCAGTCT GGACCTGAGC TGGTAAAGCC TGGGGCTTCA GTGAAGATAT   60

CCTGCAAGGC TTCTGGATAC ACATTCACTG ACTACTACAT GCACTGGGTG AAGCAGAAGC   120

CTGGGCAGGG CCTTGAGTGG ATTGGAGAGA TTTATCCTGG AAGTGGTAAT ACTTACTACA   180

ATGAGAAGTT CAAGGGYAAG GCCTCACTGA CTGCAGACAA ATCCTCCAGC ACAGCCTACA   240

TGCAGCTCAG CAGCCTGACA TCTGAGGACT CTGCAGTCTA TTTCTGTGCA AGACGTTACT   300

(2) INFORMATION FOR SEQ ID NO:24:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 46 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA   46

(2) INFORMATION FOR SEQ ID NO:25:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 295 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGGTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG   60

TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG   120

CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC   180

ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC   240

ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGAG   295

(2) INFORMATION FOR SEQ ID NO:26:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA   46

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 294 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAGGTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG   60

TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG   120

CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC   180

ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC   240

ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA   294

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA   46

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 294 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

14

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG   60

TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG   120

CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC   180

ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC   240

ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA   294

(2) INFORMATION FOR SEQ ID NO:30:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 46 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA   46

(2) INFORMATION FOR SEQ ID NO:31:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 296 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGTCCAAC TGCAGCAGCC TGGTGCTGAG CTTGTGAAGC CTGGGGCCTC AGTGAAGCTG   60

TCCTGCAAGG CTTCTGGCTA CACTTTCACC AGCTACTGGA TAAACTGGGT GAAGCAGAGG   120

CCTGGACAAG GCCTTGAGTG GATTGGAAAT ATTTATCCTG GTAGTAGTAG TACTAACTAC   180

AATGAGAAGT TCAAGAGCAA GGCCACACTG ACTGTAGACA CATCCTCCAG CACAGCCTAC   240

ATGCAGCTCA GCAGCCTGAC ATCTGACGAC TCTGCGGTCT ATTATTGTGC AAGACG   296

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA   46

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 9
        (D) OTHER INFORMATION: /note= "May also be the amino acid
arginine(R)"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 15
        (D) OTHER INFORMATION: /note= "May also be the amino acid
glutamine(E)"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 16
        (D) OTHER INFORMATION: /note= "May also be the amino acid
serine(S)"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 19
        (D) OTHER INFORMATION: /note= "May also be the amino acid
proline(P)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

    Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
    1   5   10   15

    Arg Pro Ala Pro
        20

(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 12
        (D) OTHER INFORMATION: /note= "May also be the amino acid
arginine(R)"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 18
        (D) OTHER INFORMATION: /note= "May also be the amino acid
glutamine(E)"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 19
        (D) OTHER INFORMATION: /note= "May also be the amino acid
serine(S)"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 22
        (D) OTHER INFORMATION: /note= "May also be the amino acid
proline(P)"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION: 2
        (D) OTHER INFORMATION: /note= "May also be the amino acid
proline(P)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

    Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala
    1   5   10   15

    Pro Asp Thr Arg Pro Ala Pro
               20

(2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1   5   10   15

(2) INFORMATION FOR SEQ ID NO:36:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: misc_difference
        (B) LOCATION: replace(30, "")
        (D) OTHER INFORMATION: /note= "N represents the nucleotide
  Inosine"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCAAGCTTC CAGGGRCCAR KGGATARACN GRTGG   35

(2) INFORMATION FOR SEQ ID NO:37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGAATTCAT GRAATGSASC TGGGTYWTYC TCTT   34

(2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAATACGACT CACTATAGGG   20

(2) INFORMATION FOR SEQ ID NO:39:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 19 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTTTTCCCAG TCACGACGT   19

(2) INFORMATION FOR SEQ ID NO:40:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 42 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGNWTC TT   42

(2) INFORMATION FOR SEQ ID NO:41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA   30

(2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGATGGAAG GGCCCAAC   18

(2) INFORMATION FOR SEQ ID NO:43:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 20 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATTGATGCA TATCATTACC   20

(2) INFORMATION FOR SEQ ID NO:44:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 20 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTTATCGATG TCGAATAGCC   20

(2) INFORMATION FOR SEQ ID NO:45:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 24 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTGCTGCAGA TTGAGTACTG TTCT   24

(2) INFORMATION FOR SEQ ID NO:46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Ser
                20                  25                  30

Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile
                35                  40                  45

Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
        50                  55                  60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65                  70                  75                  80

Gly Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 118 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1   5   10   15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
            85   90   95

Ala Arg Gly Xaa Xaa Xaa Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

Ser Val Thr Val Ser Ser
        115

(2) INFORMATION FOR SEQ ID NO:49:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 1..4
        (D) OTHER INFORMATION: /note= "position 54-57 of 11D10
  comparison sequence #8(Fig. 26B)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

    Ser Asp Ser Tyr
    1

(2) INFORMATION FOR SEQ ID NO:50:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids

(B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 1..9
        (D) OTHER INFORMATION: /note= "positions 118-126 of 11d10
  comparison sequence #2 and positions 100-108 of 11d10 comparison
  sequence #6 (Fig. 26B)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    1   5

(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 1..7
        (D) OTHER INFORMATION: /note= "positions 99-105 of 11D10
  comparison sequence #3 and #8 (Fig. 26B)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

    Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    1   5

(2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 1..4
        (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
  comparison sequence #12(Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Val Tyr Tyr Tyr
1

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 1..4
        (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
comparison sequence #14(Fig. 26B)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Phe Tyr Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: Region
        (B) LOCATION: 1..4
        (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
comparison sequence #15(Fig. 26B)"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Leu Phe Thr
1

(2) INFORMATION FOR SEQ ID NO:55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Ser Thr Ala Pro Pro Ala His Arg Val Thr Ser Ala Pro Glu Ser
1   5   10   15

Arg Pro Pro Pro
            20

(2) INFORMATION FOR SEQ ID NO:56:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Pro Pro Arg Ser Glu Pro Ala Ser Thr Val Arg His Ala Pro Pro
1   5   10   15

Ala Thr Ser Gly
            20

(2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Pro Asp Thr Arg Pro Pro Pro
1   5

(2) INFORMATION FOR SEQ ID NO:58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 145 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
Met Gly Thr Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
1               5                   10                  15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            20                  25                  30

Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
        35                  40                  45

Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
        50                  55                  60

Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
65                  70                  75                  80

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
                85                  90                  95

Ser Leu Glu Ser Gly Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
            100                 105                 110

Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
            115                 120                 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
        130                 135                 140

Gly
145
```